The following Listing of the Claims replaces all prior versions and all prior listings of the claims in the present application:

Listing of the Claims

1. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of ~~determine~~ the presence of a microbe ~~inhabiting~~ in a host organism, comprising the steps of:

    a) obtaining sequence information from a plurality of sequences from a host organism; and

    b) searching a database of host organism genomic sequences to determine the presence or absence of said plurality of sequences in said database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database, wherein the absence of at least one of said sequences in said database indicates that said at least one sequence is a candidate microbial sequence wherein the absence of said candidate microbial sequence in said database is indicative of ~~belonging to a microbe, thereby indicating~~ the presence of a microbe ~~inhabiting~~ in said host organism.

2. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of ~~determine~~ the presence of a microbe ~~inhabiting~~ in a host organism, comprising the steps of:

    a) obtaining sequence information from a library of genomic DNA from a host organism suspected of harboring a microbe; and

    b) searching a database of host organism genomic sequences from host organisms ~~which do not harbor the microbe~~ to determine the presence or absence of a sequence in said library in said database, wherein a sequence

is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database;
wherein the absence of said sequence indicates that said sequence is a candidate microbe sequence, ~~thereby indicating~~ which is indicative of the presence of a microbe ~~inhabiting~~ in said host organism.

3. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of ~~determine~~ the presence of a microbe ~~inhabiting~~ in a host organism, comprising the steps of:

a) obtaining sequence information from a plurality of expressed sequences from a host organism; and
b) searching a database of host organism genomic sequences to determine the presence or absence of said plurality of expressed sequences in said database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database and wherein the absence of at least one of said expressed sequences in said database indicates that said at least one sequence is a candidate sequence belonging to a microbe, ~~thereby indicating~~ which is indicative of the presence of a microbe ~~inhabiting~~ in said host organism.

4. (Currently Amended) The method according to claims 1, 2, or 3, further comprising the step of comparing said candidate sequence to a database of microbial sequences, wherein the presence of a said candidate sequence in said database of microbial sequences identifies said candidate sequence as belonging ~~wherein said candidate sequence belongs~~ to a ~~symbiotic~~ microbial organism.

5. (Currently Amended) The method according to claim 4, wherein said ~~candidate sequence belongs to~~ microbial organism is a mutualistic organism, a commensal organism, ~~or~~ a parasitic organism or a pathogenic organism.

6. (Currently Amended) The method according to claim ~~1, 2 or 3~~ 4, wherein said ~~candidate sequence belongs to~~ host organism in step (a) has a pathogenic condition and said microbial organism is an intracellular ~~a~~ pathogenic organism.

7. (Currently Amended) The method according claims 1, 2~~,~~ or 3, wherein said plurality of sequences are compared to said database of host genomic sequences simultaneously.

8. (Currently Amended) The method of claims 1, 2 or 3 wherein said host organism in step (a) has a pathogenic condition, and wherein said microbe is an intracellular pathogen ~~microbe inhabiting a host organism is an intracellular pathogen, wherein said host organism in step (a) has a pathogenic condition, and wherein said database of host organism genomic sequences in step (b) comprises genomic sequences of a plurality of host organisms not having said pathogenic condition~~.

9. (Previously Presented) The method according to claim 8, wherein said plurality of sequences are compared simultaneously with sequences in said database of host genomic sequences.

10. (Previously Presented) The method according to claim 1, wherein said sequences of said plurality of sequences are expressed sequences.

11. (Previously Presented) The method according to claim 3 or claim 10, wherein said expressed sequences are EST sequences.

12. (Previously Presented) The method according to claim 3 or claim 10, wherein said expressed sequences are cDNA sequences.

13. (Previously Presented) The method according to claim 1, 2, or 3, wherein said host organism is an animal.

14. (Original) The method according to claim 13, wherein said animal is a mammal.

15. (Original) The method according to claim 14, wherein said mammal is a human.

16. (Original) The method according to claim 13, wherein said animal is an insect, bird, or a fish.

17. (Currently Amended) The method according to claim 1, 2, or 3, wherein said host organism is ~~a microorganism,~~ a fungus, or a plant.

18. (Original) The method according to claim 11, wherein said candidate sequence is identified by comparing sequences in a database of expressed sequences with said sequences in said genomic database.

19. (Previously Presented) The method according to claim 3 or claim 10, wherein said expressed sequences are identified using a differential gene expression assay.

20. (Original) The method according to claim 19, wherein said differential gene expression assay is selected from the group consisting of SAGE, cDNA representational difference analysis, and suppression subtraction analysis.

21. (Currently Amended) The method according to claim 3 or claim 10, wherein said sequence information from a plurality of expressed sequences comprises sequences ~~candidate sequence is~~ identified using a subtractive hybridization method.

22. (Original) The method according to claim 21, wherein said subtractive hybridization method is representational difference analysis.

23. (Currently Amended) The method according to claim 1, 2, or 3, further comprising the step of using ~~wherein~~ said candidate sequence ~~is used~~ as a query sequence to search a database of microbial sequences, wherein the presence of said candidate sequence in said database of microbial sequences identifies said candidate sequence as a microbial sequence.

24. (Original) The method according to claim 23, wherein said microbial sequences include viral sequences.

25. (Previously Presented) The method according to claim 1, 2, or 3, wherein any of: vector sequences, repetitive sequences, mitochondrial sequences, non-host species sequences,

known host organism sequences, and combinations thereof are eliminated from the genomic database comprising sequences from the host organism.

26. (Previously Presented) The method according to claim 1, 2, or 3, wherein said searching is performed iteratively using progressively smaller word sizes.

27. (Canceled)

28. (Canceled)

29. (Previously Presented) The method according to claim 6, wherein said pathogen is an infectious disease organism.

30. (Previously Presented) The method according to claim 6, wherein said pathogen is associated with a pathogenic condition selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.

31. (Original) The method according to claim 30, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.

32. (Canceled)

33. (Canceled)

34. (Canceled)

35. (Canceled)

36. (Canceled)

37. (Canceled)

38. (Canceled)

39. (Canceled)

40. (Canceled)

41. (Canceled)

42. (Canceled)

43. (Canceled)

44. (Canceled)

45. (Canceled)

46. (Canceled)

47. (Canceled)

48. (Canceled)

49. (Canceled)

50. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of ~~determine~~ the presence of a microbe ~~inhabiting~~ in a host organism, comprising the steps of:

obtaining sequence information from a plurality of expressed sequences from a human host organism; and

searching a database of host organism genomic sequences to determine the presence or absence of the plurality of expressed sequences in the database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of sequence identical to a sequence in said database, wherein the absence of an expressed sequence in the database identifies the expressed sequence as a candidate microbial ~~microbe~~ sequence, wherein the absence of said candidate microbial sequence in said database is indicative of ~~thereby indicating~~ the presence of a microbe ~~inhabiting~~ in said host organism.

51. (Original) The method according to claim 50, wherein said plurality of sequences are from a library of sequences.

52. (Canceled)

53. (Canceled)

54. (Currently Amended) The method according to claim ~~53~~ 51, wherein said library comprises human sequences from one or more humans having a pathological condition.

55. (Original) The method according to claim 54, wherein said pathological condition is a disease selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.

56. (Original) The method according to claim 55, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.

57. (Original) The method according to claim 50, wherein said step of obtaining sequence information comprises sequencing expressed sequences cloned in a library of expressed sequences.

58. (Currently Amended) A method of using a computer system to evaluate nucleic acid sequences of a non-microbial host organism for the presence of a candidate microbial sequence indicative of ~~determine~~ the presence of a microbe ~~inhabiting~~ in a host organism, comprising the steps of:

obtaining expressed sequence information from a plurality of sequences from at least one non-microbial host organism; and

searching a database of microbial sequences from a library of expressed sequences to determine the presence or absence of said plurality of sequences from at least one non-microbial host organism in the database, wherein a sequence is present in said database if it contains 20 consecutive nucleotides of

sequence identical to a sequence in said database, wherein the presence of an expressed sequence from said at least one non-microbial host organism in the database identifies the expressed sequence as a candidate microbe sequence, wherein the presence of said candidate microbial sequence in said database is indicative of ~~thereby indicating~~ the presence of a microbe ~~inhabiting~~ in said host organism.

59. (Canceled)

60. (Original) The method according to claim 58, wherein said library of expressed sequences comprises sequences from one or more humans having a pathological condition.

61. (Original) The method according to claim 60, wherein said pathological condition is an infectious disease.

62. (Previously Presented) The method according to claim 8, wherein said pathogen is an infectious disease organism.

63. (Previously Presented) The method according to claim 8, wherein said pathogen is associated with a pathogenic condition selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.

64. (Previously Presented) The method according to claim 63, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.